

RAW SEQUENCE LISTING

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Application Serial Number: 10/551,550
Source: FwP
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RAW SEQUENCE LISTING

DATE: 02/21/2007

PATENT APPLICATION: US/10/551,550

TIME: 14:20:03

Input Set : A:\10-551,550 Sequence Listing.txt
 Output Set: N:\CRF4\02212007\J551550.raw

3 <110> APPLICANT: Seikagaku Corporation
 5 <120> TITLE OF INVENTION: Catalyst for cleaving sugar chain
 7 <130> FILE REFERENCE: Q90646
 9 <140> CURRENT APPLICATION NUMBER: US 10/551,550
 10 <141> CURRENT FILING DATE: 2005-09-30
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/004695
 13 <151> PRIOR FILING DATE: 2004-03-31
 15 <150> PRIOR APPLICATION NUMBER: JP 2003-097301
 16 <151> PRIOR FILING DATE: 2003-03-31
 18 <150> PRIOR APPLICATION NUMBER: JP 2003-113965
 19 <151> PRIOR FILING DATE: 2003-04-18
 21 <160> NUMBER OF SEQ ID NOS: 2
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1308
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1308)
 33 <400> SEQUENCE: 1
 34 atg gca gcc cac ctg ctt ccc atc tgc gcc ctc ttc ctg acc tta ctc 48
 35 Met Ala Ala His Leu Leu Pro Ile Cys Ala Leu Phe Leu Thr Leu Leu
 36 1 5 10 15
 37 gat atg gcc caa ggc ttt agg ggc ccc ttg cta ccc aac cgg ccc ttc 96
 38 Asp Met Ala Gln Gly Phe Arg Gly Pro Leu Leu Pro Asn Arg Pro Phe
 39 20 25 30
 40 acc acc gtc tgg aat gca aac acc cag tgg tgc ctg gag agg cac ggt 144
 41 Thr Thr Val Trp Asn Ala Asn Thr Gln Trp Cys Leu Glu Arg His Gly
 42 35 40 45
 43 gtg gac gtg gat gtc agt gtc ttc gat gtg gta gcc aac cca ggg cag 192
 44 Val Asp Val Asp Val Ser Val Phe Asp Val Val Ala Asn Pro Gly Gln
 45 50 55 60
 46 acc ttc cgc ggc cct gac atg aca att ttc tat agc tcc cag ctg ggc 240
 47 Thr Phe Arg Gly Pro Asp Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly
 48 65 70 75 80
 49 acc tac ccc tac tac acg ccc act ggg gag cct gtg ttt ggt ggt ctg 288
 50 Thr Tyr Pro Tyr Tyr Thr Pro Thr Gly Glu Pro Val Phe Gly Gly Leu
 51 85 90 95
 52 ccc cag aat gcc agc ctg att gcc cac ctg gcc cgc aca ttc cag gac 336
 53 Pro Gln Asn Ala Ser Leu Ile Ala His Leu Ala Arg Thr Phe Gln Asp
 54 100 105 110
 55 atc ctg gct gcc ata cct gct cct gac ttc tca ggg ctg gca gtc atc 384

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56	Ile	Leu	Ala	Ala	Ile	Pro	Ala	Pro	Asp	Phe	Ser	Gly	Leu	Ala	Val	Ile
57		115				120				125						
58	gac	tgg	gag	gca	tgg	cgc	cca	cgc	tgg	gcc	ttc	aac	tgg	gac	acc	aag
59	Asp	Trp	Glu	Ala	Trp	Arg	Pro	Arg	Trp	Ala	Phe	Asn	Trp	Asp	Thr	Lys
60		130				135				140						
61	gac	att	tac	cgg	cag	cgc	tca	cggt	gca	cag	gca	cag	cac	cct		
62	Asp	Ile	Tyr	Arg	Gln	Arg	Ser	Arg	Ala	Leu	Val	Gln	Ala	Gln	His	Pro
63	145				150				155				160			
64	gat	tgg	cca	gct	cct	cag	gtg	gag	gca	gta	gcc	cag	gac	cag	ttc	cag
65	Asp	Trp	Pro	Ala	Pro	Gln	Val	Glu	Ala	Val	Ala	Gln	Asp	Gln	Phe	Gln
66						165			170				175			
67	gga	gct	gca	cgg	gcc	tgg	atg	gca	ggc	acc	ctc	cag	ctg	ggg	cgg	gca
68	Gly	Ala	Ala	Arg	Ala	Trp	Met	Ala	Gly	Thr	Leu	Gln	Leu	Gly	Arg	Ala
69						180			185				190			
70	ctg	cgt	cct	cgc	ggc	ctc	tgg	ggc	ttc	tat	ggc	ttc	cct	gac	tgc	tac
71	Leu	Arg	Pro	Arg	Gly	Leu	Trp	Gly	Phe	Tyr	Gly	Phe	Pro	Asp	Cys	Tyr
72						195			200				205			
73	aac	tat	gac	ttt	cta	agc	ccc	aac	tac	acc	ggc	cag	tgc	cca	tca	ggc
74	Asn	Tyr	Asp	Phe	Leu	Ser	Pro	Asn	Tyr	Thr	Gly	Gln	Cys	Pro	Ser	Gly
75						210			215				220			
76	atc	cgt	gcc	caa	aat	gac	cag	cta	ggg	tgg	ctg	tgg	ggc	cag	agc	cgt
77	Ile	Arg	Ala	Gln	Asn	Asp	Gln	Leu	Gly	Trp	Leu	Trp	Gly	Gln	Ser	Arg
78	225					230			235				240			
79	gcc	ctc	tat	ccc	agc	atc	tac	atg	ccc	gca	gtg	ctg	gag	ggc	aca	ggg
80	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Met	Pro	Ala	Val	Leu	Glu	Gly	Thr	Gly
81						245			250				255			
82	aag	tca	cag	atg	tat	gtg	caa	cac	cgt	gtg	gcc	gag	gca	ttc	cgt	gtg
83	Lys	Ser	Gln	Met	Tyr	Val	Gln	His	Arg	Val	Ala	Glu	Ala	Phe	Arg	Val
84						260			265				270			
85	gct	gtg	gct	ggt	gac	ccc	aat	ctg	ccg	gtg	ctg	ccc	tat	gtc	cag	
86	Ala	Val	Ala	Ala	Gly	Asp	Pro	Asn	Leu	Pro	Val	Leu	Pro	Tyr	Val	Gln
87						275			280				285			
88	atc	ttc	tat	gac	acg	aca	aac	cac	ttt	ctg	ccc	ctg	gat	gag	ctg	gag
89	Ile	Phe	Tyr	Asp	Thr	Asn	His	Phe	Leu	Pro	Leu	Asp	Glu	Leu	Glu	
90						290			295				300			
91	cac	agc	ctg	ggg	gag	agt	gct	gcc	cag	ggg	gca	gct	gga	gtg	gtg	ctc
92	His	Ser	Leu	Gly	Glu	Ser	Ala	Ala	Gln	Gly	Ala	Ala	Gly	Val	Val	Leu
93	305					310			315				320			
94	tgg	gtg	agc	tgg	gaa	aat	aca	aga	acc	aag	gaa	tca	tgt	cag	gcc	atc
95	Trp	Val	Ser	Trp	Glu	Asn	Thr	Arg	Thr	Lys	Glu	Ser	Cys	Gln	Ala	Ile
96						325			330				335			
97	aag	gag	tat	atg	gac	act	aca	ctg	ggg	ccc	ttc	atc	ctg	aac	gtg	acc
98	Lys	Glu	Tyr	Met	Asp	Thr	Leu	Gly	Pro	Phe	Ile	Leu	Asn	Val	Thr	
99						340			345				350			
100	agt	ggg	gcc	ctt	ctc	tgc	agt	caa	gcc	ctg	tgc	tcc	ggc	cat	ggc	cgc
101	Ser	Gly	Ala	Leu	Leu	Cys	Ser	Gln	Ala	Leu	Cys	Ser	Gly	His	Gly	Arg
102						355			360				365			
103	tgt	gtc	cgc	cgc	acc	agc	cac	ccc	aaa	gcc	ctc	ctc	ctc	ctt	aac	cct
104	Cys	Val	Arg	Arg	Thr	Ser	His	Pro	Lys	Ala	Leu	Leu	Leu	Asn	Pro	

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105	370	375	380	
106	gcc agt ttc tcc atc cag ctc acg cct ggt ggt ggg ccc ctg agc ctg			1200
107	Ala Ser Phe Ser Ile Gln Leu Thr Pro Gly Gly Pro Leu Ser Leu			
108	385	390	395	400
109	cgg ggt gcc ctc tca ctt gaa gat cag gca cag atg gct gtg gag ttc			1248
110	Arg Gly Ala Leu Ser Leu Glu Asp Gln Ala Gln Met Ala Val Glu Phe			
111	405	410	415	
112	aaa tgt cga tgc tac cct ggc tgg cag gca ccg tgg tgt gag cgg aag			1296
113	Lys Cys Arg Cys Tyr Pro Gly Trp Gln Ala Pro Trp Cys Glu Arg Lys			
114	420	425	430	
115	agc atg tgg tga			1308
116	Ser Met Trp			
117	435			
120	<210> SEQ ID NO: 2			
121	<211> LENGTH: 435			
122	<212> TYPE: PRT			
123	<213> ORGANISM: Homo sapiens			
125	<400> SEQUENCE: 2			
126	Met Ala Ala His Leu Leu Pro Ile Cys Ala Leu Phe Leu Thr Leu Leu			
127	1	5	10	15
128	Asp Met Ala Gln Gly Phe Arg Gly Pro Leu Leu Pro Asn Arg Pro Phe			
129	20	25	30	
130	Thr Thr Val Trp Asn Ala Asn Thr Gln Trp Cys Leu Glu Arg His Gly			
131	35	40	45	
132	Val Asp Val Asp Val Ser Val Phe Asp Val Val Ala Asn Pro Gly Gln			
133	50	55	60	
134	Thr Phe Arg Gly Pro Asp Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly			
135	65	70	75	80
136	Thr Tyr Pro Tyr Tyr Pro Thr Gly Glu Pro Val Phe Gly Gly Leu			
137	85	90	95	
138	Pro Gln Asn Ala Ser Leu Ile Ala His Leu Ala Arg Thr Phe Gln Asp			
139	100	105	110	
140	Ile Leu Ala Ala Ile Pro Ala Pro Asp Phe Ser Gly Leu Ala Val Ile			
141	115	120	125	
142	Asp Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Thr Lys			
143	130	135	140	
144	Asp Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Ala Gln His Pro			
145	145	150	155	160
146	Asp Trp Pro Ala Pro Gln Val Glu Ala Val Ala Gln Asp Gln Phe Gln			
147	165	170	175	
148	Gly Ala Ala Arg Ala Trp Met Ala Gly Thr Leu Gln Leu Gly Arg Ala			
149	180	185	190	
150	Leu Arg Pro Arg Gly Leu Trp Gly Phe Tyr Gly Phe Pro Asp Cys Tyr			
151	195	200	205	
152	Asn Tyr Asp Phe Leu Ser Pro Asn Tyr Thr Gly Gln Cys Pro Ser Gly			
153	210	215	220	
154	Ile Arg Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg			
155	225	230	235	240
156	Ala Leu Tyr Pro Ser Ile Tyr Met Pro Ala Val Leu Glu Gly Thr Gly			

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157 245 250 255
158 Lys Ser Gln Met Tyr Val Gln His Arg Val Ala Glu Ala Phe Arg Val
159 260 265 270
160 Ala Val Ala Ala Gly Asp Pro Asn Leu Pro Val Leu Pro Tyr Val Gln
161 275 280 285
162 Ile Phe Tyr Asp Thr Thr Asn His Phe Leu Pro Leu Asp Glu Leu Glu
163 290 295 300
164 His Ser Leu Gly Glu Ser Ala Ala Gln Gly Ala Ala Gly Val Val Leu
165 305 310 315 320
166 Trp Val Ser Trp Glu Asn Thr Arg Thr Lys Glu Ser Cys Gln Ala Ile
167 325 330 335
168 Lys Glu Tyr Met Asp Thr Thr Leu Gly Pro Phe Ile Leu Asn Val Thr
169 340 345 350
170 Ser Gly Ala Leu Leu Cys Ser Gln Ala Leu Cys Ser Gly His Gly Arg
171 355 360 365
172 Cys Val Arg Arg Thr Ser His Pro Lys Ala Leu Leu Leu Asn Pro
173 370 375 380
174 Ala Ser Phe Ser Ile Gln Leu Thr Pro Gly Gly Pro Leu Ser Leu
175 385 390 395 400
176 Arg Gly Ala Leu Ser Leu Glu Asp Gln Ala Gln Met Ala Val Glu Phe
177 405 410 415
178 Lys Cys Arg Cys Tyr Pro Gly Trp Gln Ala Pro Trp Cys Glu Arg Lys
179 420 425 430
180 Ser Met Trp
181 435

VERIFICATION SUMMARY

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DATE: 02/21/2007

TIME: 14:20:04

Input Set : A:\10-551,550 Sequence Listing.txt

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